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SUBSTITUTE SEQUENCE LISTING

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<120> THERMAL TOLERANT CELLULASE FROM ACIDOTHERMUS
CELLULOLYTICUS

<130> 40197.6WOOI

<140> 09/917,383

<141> 2001-07-28

<160> 14

<170> Patent In Version 3.1

<210> 1

<211> 1228

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Segment of
GuxA

<400> 1

Met Glu Arg Thr Gln Gln Ser Gly Arg Asn Cys Arg Tyr Gln Arg Gly
1 5 10 15

Thr Thr Arg Met Pro Ala Ile Ser Lys Arg Leu Arg Ala Gly Val Leu
20 25 30

Ala Gly Ala Val Ser Ile Ala Ala Ser Ile Val Pro Leu Ala Met Gln
35 40 45

His Pro Ala Ile Ala Ala Thr His Val Asp Asn Pro Tyr Ala Gly Ala
50 55 60

Thr Phe Phe Val Asn Pro Tyr Trp Ala Gln Glu Val Gln Ser Glu Ala
65 70 75 80

Ala Asn Gln Thr Asn Ala Thr Leu Ala Ala Lys Met Arg Val Val Ser
85 90 95

Thr Tyr Ser Thr Ala Val Trp Met Asp Arg Ile Ala Ala Ile Asn Gly
100 105 110

Val Asn Gly Gly Pro Gly Leu Thr Thr Tyr Leu Asp Ala Ala Leu Ser
115 120 125

Gln Gln Gln Gly Thr Thr Pro Glu Val Ile Glu Ile Val Ile Tyr Asp
130 135 140

Leu Pro Gly Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu Leu Pro
145 150 155 160

Ala Thr Ala Ala Gly Leu Gln Thr Tyr Glu Thr Gln Tyr Ile Asp Pro
165 170 175

Ile Ala Ser Ile Leu Ser Asn Pro Lys Tyr Ser Ser Leu Arg Ile Val
180 185 190

Thr Ile Ile Glu Pro Asp Ser Leu Pro Asn Ala Val Thr Asn Met Ser
195 200 205

Ile Gln Ala Cys Ala Thr Ala Val Pro Tyr Tyr Glu Gln Gly Ile Glu
210 215 220

Tyr Ala Leu Thr Lys Leu His Ala Ile Pro Asn Val Tyr Ile Tyr Met
225 230 235 240

Asp Ala Ala His Ser Gly Trp Leu Gly Trp Pro Asn Asn Ala Ser Gly
245 250 255

Tyr Val Gln Glu Val Gln Lys Val Leu Asn Ala Ser Ile Gly Val Asn
260 265 270

Gly Ile Asp Gly Phe Val Thr Asn Thr Ala Asn Tyr Thr Pro Leu Lys
275 280 285

Glu Pro Phe Met Thr Ala Thr Gln Gln Val Gly Gly Gln Pro Val Glu
290 295 300

Ser Ala Asn Phe Tyr Gln Trp Asn Pro Asp Ile Asp Glu Ala Asp Tyr
305 310 315 320

Ala Val Asp Leu Tyr Ser Arg Leu Val Ala Ala Gly Phe Pro Ser Ser
325 330 335

Ile Gly Met Leu Ile Asp Thr Leu Arg Asn Gly Trp Gly Gly Pro Asn
340 345 350

Glu Pro Thr Gly Pro Ser Thr Ala Thr Asp Val Asn Thr Phe Val Asn
355 360 365

Gln Ser Lys Ile Asp Leu Arg Gln His Arg Gly Leu Trp Cys Asn Gln
370 375 380

Asn Gly Ala Gly Leu Gly Gln Pro Pro Gln Ala Ser Pro Thr Asp Phe
385 390 395 400

Pro Asn Ala His Leu Asp Ala Tyr Val Trp Ile Lys Pro Pro Gly Glu
405 410 415

Ser Asp Gly Thr Ser Ala Ala Ser Asp Pro Thr Thr Gly Lys Lys Ser
420 425 430

Asp Pro Met Cys Asp Pro Thr Tyr Thr Thr Ser Tyr Gly Val Leu Thr
435 440 445

Asn Ala Leu Pro Asn Ser Pro Ile Ala Gly Gln Trp Phe Pro Ala Gln
450 455 460

Phe Asp Gln Leu Val Ala Asn Ala Arg Pro Ala Val Pro Thr Ser Thr
465 470 475 480

Ser Ser Ser Pro Pro Pro Pro Pro Ser Ala Ser Pro Ser
485 490 495

Pro Ser Pro Ser Pro Ser Pro Ser Ser Ser Pro Ser Pro Ser Pro Ser
500 505 510

Pro Ser Ser Ser Pro Ser Pro Ser Pro Ser Pro Ser Pro Ser Pro Ser
515 520 525

Ser Ser Pro Ser Pro Ser Pro Ser Ser Ser Pro Ser Pro Ser Pro Ser
530 535 540

Pro Ser Pro Ser Pro Ser Ser Ser Pro Ser Pro Ser Pro Ser Ser Ser
545 550 555 560

Pro Ser Pro Ser Pro Ser Pro Ser Pro Ser Pro Ser Ser Ser Pro Ser
565 570 575

Pro Ser Pro Thr Ser Ser Pro Val Ser Gly Gly Leu Lys Val Gln Tyr
580 585 590

Lys Asn Asn Asp Ser Ala Pro Gly Asp Asn Gln Ile Lys Pro Gly Leu
595 600 605

Gln Leu Val Asn Thr Gly Ser Ser Ser Val Asp Leu Ser Thr Val Thr
610 615 620

Val Arg Tyr Trp Phe Thr Arg Asp Gly Gly Ser Ser Thr Leu Val Tyr
625 630 635 640

Asn Cys Asp Trp Ala Ala Met Gly Cys Gly Asn Ile Arg Ala Ser Phe
645 650 655

Gly Ser Val Asn Pro Ala Thr Pro Thr Ala Asp Thr Tyr Leu Gln Leu
660 665 670

Ser Phe Thr Gly Gly Thr Leu Ala Ala Gly Gly Ser Thr Gly Glu Ile
675 680 685

Gln Asn Arg Val Asn Lys Ser Asp Trp Ser Asn Phe Thr Glu Thr Asn
690 695 700

Asp Tyr Ser Tyr Gly Thr Asn Thr Thr Phe Gln Asp Trp Thr Lys Val
705 710 715 720

Thr Val Tyr Val Asn Gly Val Leu Val Trp Gly Thr Glu Pro Ser Gly
725 730 735

Thr Ser Pro Ser Pro Thr Pro Ser Pro Ser Pro Ser Pro Ser Pro Ser
740 745 750

Pro Gly Gly Asp Val Thr Pro Pro Ser Val Pro Thr Gly Leu Val Val
755 760 765

Thr Gly Val Ser Gly Ser Ser Val Ser Leu Ala Trp Asn Ala Ser Thr
770 775 780

Asp Asn Val Gly Val Ala His Tyr Asn Val Tyr Arg Asn Gly Val Leu
785 790 795 800

Val Gly Gln Pro Thr Val Thr Ser Phe Thr Asp Thr Gly Leu Ala Ala
805 810 815

Gly Thr Ala Tyr Thr Tyr Thr Val Ala Ala Val Asp Ala Ala Gly Asn
820 825 830

Thr Ser Ala Pro Ser Thr Pro Val Thr Ala Thr Thr Thr Ser Pro Ser
835 840 845

Pro Ser Pro Thr Pro Thr Gly Thr Thr Val Thr Asp Cys Thr Pro Gly
850 855 860

Pro Asn Gln Asn Gly Val Thr Ser Val Gln Gly Asp Glu Tyr Arg Val
865 870 875 880

Gln Thr Asn Glu Trp Asn Ser Ser Ala Gln Gln Cys Leu Thr Ile Asn
885 890 895

Thr Ala Thr Gly Ala Trp Thr Val Ser Thr Ala Asn Phe Ser Gly Gly
900 905 910

Thr Gly Gly Ala Pro Ala Thr Tyr Pro Ser Ile Tyr Lys Gly Cys His
915 920 925

Trp Gly Asn Cys Thr Thr Lys Asn Val Gly Met Pro Ile Gln Ile Ser
930 935 940

Gln Ile Gly Ser Ala Val Thr Ser Trp Ser Thr Thr Gln Val Ser Ser
945 950 955 960

Gly Ala Tyr Asp Val Ala Tyr Asp Ile Trp Thr Asn Ser Thr Pro Thr
965 970 975

Thr Thr Gly Gln Pro Asn Gly Thr Glu Ile Met Ile Trp Leu Asn Ser
980 985 990

Arg Gly Gly Val Gln Pro Phe Gly Ser Gln Thr Ala Thr Gly Val Thr
995 1000 1005

Val Ala Gly His Thr Trp Asn Val Trp Gln Gly Gln Gln Thr Ser Trp
1010 1015 1020

Lys Ile Ile Ser Tyr Val Leu Thr Pro Gly Ala Thr Ser Ile Ser Asn
1025 1030 1035 1040

Leu Asp Leu Lys Ala Ile Phe Ala Asp Ala Ala Arg Gly Ser Leu
1045 1050 1055

Asn Thr Ser Asp Tyr Leu Leu Asp Val Glu Ala Gly Phe Glu Ile Trp
1060 1065 1070

Gln Gly Gly Gln Gly Leu Gly Ser Asn Ser Phe Ser Val Ser Val Thr
1075 1080 1085

Ser Gly Thr Ser Ser Pro Thr Pro Ser Pro Ser Pro Thr Pro Thr Pro
1090 1095 1100

Ser Pro Thr Pro Thr Pro Ser Pro Ser Pro Thr Pro Ser Pro Ser Pro
1105 1110 1115 1120

Thr Ser Ser Pro Ser Ser Ser Gly Val Ala Cys Arg Ala Thr Tyr Val
1125 1130 1135

Val Asn Ser Asp Trp Gly Ser Gly Phe Thr Ala Thr Val Thr Val Thr
1140 1145 1150

Asn Thr Gly Ser Arg Ala Thr Asn Gly Trp Thr Val Ala Trp Ser Phe
1155 1160 1165

Gly Gly Asn Gln Thr Val Thr Asn Tyr Trp Asn Thr Ala Leu Thr Gln
1170 1175 1180

Ser Gly Ala Ser Val Thr Ala Thr Asn Leu Ser Tyr Asn Asn Val Ile
1185 1190 1195 1200

Gln Pro Gly Gln Ser Thr Thr Phe Gly Phe Asn Gly Ser Tyr Ser Gly
1205 1210 1215

Thr Asn Ala Ala Pro Thr Leu Ser Cys Thr Ala Ser
1220 1225

<210> 2

<211> 3687

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Segment of
GuxA

<400> 2

| | |
|---|-----|
| atggagcgaa cccaacaatc cggacggaac tgcaggtacc agagaggaac gacacgaatg | 60 |
| cccgccatct caaaacggct gcgagccggc gtcctcgccg gggcggtgag catcgagcc | 120 |
| tccatctgac cgctggcgat gcagcatcct gccatcgccg cgacgcacgt cgacaatccc | 180 |
| tatgcgggag cgaccttctt cgtcaaccgc tactggcgcg aagaagtaca gagcgaagcg | 240 |
| gcgaaccaga ccaatgccac tctgcagcg aaaatgcgcg tcgtttccac atattcgacg | 300 |
| gccgtctgga tggaccgcat cgctgcgac aacggcgta acggcggacc cggcttgacg | 360 |
| acatatctgg acgccgccct ctcccagcag cagggaacca cccctgaagt cattgagatt | 420 |
| gtcatctacg atctgcggg acgcgactgc gcgcgctcg cctccaacgg cgaactgcc | 480 |
| gtacggcag caggtttgca gacctatgaa acgcagtaca tcgatccgat tgcgagtac | 540 |
| ctgagcaatc cgaagtactc cagcctgagg atcgtgacga tcattgagcc ggactcgctg | 600 |
| ccaaacgcgg tcaccaatat gagcattcaa gcgtgtgcaa cggcggtgcc gtattacgag | 660 |
| caaggcatcg agtacgcgct cagcaaatg cagccattc cgaacgtgta catctacatg | 720 |
| gacgcgccc actccggtg gcttgggtgg cccaataatg ccagcggata cgtacaggaa | 780 |
| gtccagaagg tctcaacgc gagcatcggg gtcaacggca tcgacggctt cgtcaccaac | 840 |

| | |
|--|------|
| acggcgaatt acacgccgtt gaaggagccg ttcattgaccg ccacccagca ggtcggcgga | 900 |
| cagccggtgg agtcggcgaa ttctaccag tggaaactcg acatcgacga agccgactac | 960 |
| gcggttgact tctactcgcg gctcgtcgcc gctggcttc caagcagcat cggcatgctc | 1020 |
| atcgacacct tacgcaacgg ttgggtgggt ccgaacgaac caacaggccc gagcaccgcg | 1080 |
| accgatgtca acaccttctg caaccagtcg aagattgacc ttccgcagca ccgcggcctg | 1140 |
| tgttgcaacc agaacgggtg gggcctcggc cagcccgccg aggcaagccc gacggacttc | 1200 |
| ccgaacgcgc acctcgacgc gtaigtctgg atcaagccgc cgggtgagtc ggacggcaca | 1260 |
| agcgtgcca gcgatccgac aactggcaag aagtcggacc ccatgtgca cccgacgtac | 1320 |
| acgacgtcgt acgggggtact gaccaacgcg ttaccgaact ccccgatcgc cggccagtgg | 1380 |
| ttccggcgcg agtttgacca gctgtcgcg aacgcacggc cagcgggtgc gacgtcgacc | 1440 |
| agctcgagcc cgcgcctcc gccgccgagt ccgtcggctt cgcgagtcg gagccccagt | 1500 |
| ccgagcccga gcagtcgccc atcgccgtcg ccgtctccga gtcgagccc gtctccgtcg | 1560 |
| ccgagcccga gtccgagccc gtagtctcg ccgtcgccgt ctccgagtc gagccccgt | 1620 |
| ccgtcgccga gcccagtc gagccccagt agtcgccgt cgccgtctcc gagctcgagc | 1680 |
| ccgtctccgt cgcgagccc gactccgagc ccgagtagct cgccgtcgcc gtctccgacg | 1740 |
| tcgtcgccgg tgcgggtgg gctgaagggt cagtacaaga acaatgattc ggcgcgggt | 1800 |
| gataaccaga tcaaaccggg tctccagttg gtgaataccg ggtcgtcgtc ggtgatttg | 1860 |
| tcgacgggtga cggtcgggt cgtgttcacc cgggatgggt ggtcgtcgac actggtgtac | 1920 |
| aactgtgact gggcgccgtt ggggtgtggg aatatccgcg cctcgttcgg ctccgtgaac | 1980 |
| ccggcgacgc cgacggcgga cactacctg cagtgtcgt tcaatgggtg aacgttgcc | 2040 |
| gctggtgggt cgacgggtga gattcaaac cgggtgaata agagtactg gtcgaattc | 2100 |
| accgagacca atgactact gtaggggacg aacaccacct tccaggactg gacgaagggt | 2160 |
| acgggtgacg tcaacggcgt gttggtgtgg gggactgaac cgtccggcac cagccccagc | 2220 |
| cccacacat ccccgagccc gagccccagc ccgagcccgg gtggggatgt gacccgccc | 2280 |
| agtgtgccga cgggcttggg ggtgacgggg gtgagtggtg cgtcgggtgc gttggcgtgg | 2340 |
| aatgcgtcga cggataacgt gggggtggcg cattacaacg tgtaccgcaa cggggtgtg | 2400 |
| gtgggccagc cgacggtgac ctctgtcacc gacacgggtt tggccgcggg aaccgcgtac | 2460 |
| acctacacgg tggccgcggg ggacgtcgc ggtaaacact ccgccccatc ccccccgtc | 2520 |
| accgccacca ccacgagtc cagccccagc cccacgccga cggggaccac ggtcaccgac | 2580 |
| tgcacgccc gtcctaacca gaatgtgtg accagcgtgc agggcgacga ataccgggtg | 2640 |
| cagaccaatg agtgaattc gtcggcccag cagtgcctca ccatcaatac cgcgaccggt | 2700 |
| gcctggacgg tgagcactgc gaactcagc ggtgggaccg gcggtgcgcc cgcgacgtat | 2760 |
| ccgtcgatct acaagggctg cactggggc aactgcacca cgaagaacgt cgggatgccg | 2820 |
| attcagatca gtcagattg ttccgctgtg acgtcgtgga gtacgacga ggtgtcgtc | 2880 |
| ggcgcgtatg acgtggccta cgacatttg acgaacagta cccaacgac aaccggtcag | 2940 |
| ccaaacggta ccgaaatcat gatttgctg aattcgctg gtgggtgca gccgttcggg | 3000 |
| tcgacagacg cgacgggtgt gacggtcgt ggtcacagt ggaatgtctg gcagggtcag | 3060 |
| cagacctcgt ggaagattat ttctacgtc ctgaccccc gtgcgacgtc gatcagtaat | 3120 |
| ctggattga aggcgattt cgcggacgcc gcggcacgcg ggtcgtcaa cactccgat | 3180 |
| tactgtctg acgttaggc cgggttgag atctggcaag gtgtcaggg cctgggcagc | 3240 |
| aactcgttca cgtctccgt gacgagcgc acgtccagcc cgacaccgag cccgagccc | 3300 |
| acgccgacac cgagcccag gccgaacccg tctccgagcc cgaccccgtc gccgagtcg | 3360 |
| accagctgc cgtcgtcgtc ggggtgtggc tgcggggcga cgtatgtgt gaatagtgt | 3420 |
| tgggttctg ggtttacgc gacggtgacg gtgacgaata cgggagccg ggcgacgaac | 3480 |
| gggtggacgg tggcgtggtc gttgtgtgg aatcagacgg tcacgaacta ctggaacact | 3540 |
| gcgtgaccc aatcaggtgc atcgtgacg gcgacgaacc tgagttacaa caacgtgatc | 3600 |
| caaccgggtc agtcgaccac ctccgattc aacggaagt actcaggaac aaacgccgcg | 3660 |
| ccgacgtca gtcgacagc cagctga | 3687 |

<210> 3

<211> 53

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Segment of
GuxA

<400> 3

Met Glu Arg Thr Gln Gln Ser Gly Arg Asn Cys Arg Tyr Gln Arg Gly
1 5 10 15

Thr Thr Arg Met Pro Ala Ile Ser Lys Arg Leu Arg Ala Gly Val Leu
20 25 30

Ala Gly Ala Val Ser Ile Ala Ala Ser Ile Val Pro Leu Ala Met Gln
35 40 45

His Pro Ala Ile Ala
50

<210> 4

<211> 423

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Segment of
GuxA

<400> 4

Ala Thr His Val Asp Asn Pro Tyr Ala Gly Ala Thr Phe Phe Val Asn
1 5 10 15

Pro Tyr Trp Ala Gln Glu Val Gln Ser Glu Ala Ala Asn Gln Thr Asn
20 25 30

Ala Thr Leu Ala Ala Lys Met Arg Val Val Ser Thr Tyr Ser Thr Ala
35 40 45

Val Trp Met Asp Arg Ile Ala Ala Ile Asn Gly Val Asn Gly Gly Pro
50 55 60

Gly Leu Thr Thr Tyr Leu Asp Ala Ala Leu Ser Gln Gln Gln Gly Thr
65 70 75 80

Thr Pro Glu Val Ile Glu Ile Val Ile Tyr Asp Leu Pro Gly Arg Asp
85 90 95

Cys Ala Ala Leu Ala Ser Asn Gly Glu Leu Pro Ala Thr Ala Ala Gly
100 105 110

Leu Gln Thr Tyr Glu Thr Gln Tyr Ile Asp Pro Ile Ala Ser Ile Leu
115 120 125

Ser Asn Pro Lys Tyr Ser Ser Leu Arg Ile Val Thr Ile Ile Glu Pro
130 135 140

Asp Ser Leu Pro Asn Ala Val Thr Asn Met Ser Ile Gln Ala Cys Ala
145 150 155 160

Thr Ala Val Pro Tyr Tyr Glu Gln Gly Ile Glu Tyr Ala Leu Thr Lys
165 170 175

Leu His Ala Ile Pro Asn Val Tyr Ile Tyr Met Asp Ala Ala His Ser
180 185 190

Gly Trp Leu Gly Trp Pro Asn Asn Ala Ser Gly Tyr Val Gln Glu Val
195 200 205

Gln Lys Val Leu Asn Ala Ser Ile Gly Val Asn Gly Ile Asp Gly Phe
210 215 220

Val Thr Asn Thr Ala Asn Tyr Thr Pro Leu Lys Glu Pro Phe Met Thr
225 230 235 240

Ala Thr Gln Gln Val Gly Gly Gln Pro Val Glu Ser Ala Asn Phe Tyr
245 250 255

Gln Trp Asn Pro Asp Ile Asp Glu Ala Asp Tyr Ala Val Asp Leu Tyr
260 265 270

Ser Arg Leu Val Ala Ala Gly Phe Pro Ser Ser Ile Gly Met Leu Ile
275 280 285

Asp Thr Leu Arg Asn Gly Trp Gly Gly Pro Asn Glu Pro Thr Gly Pro
290 295 300

Ser Thr Ala Thr Asp Val Asn Thr Phe Val Asn Gln Ser Lys Ile Asp
305 310 315 320

Leu Arg Gln His Arg Gly Leu Trp Cys Asn Gln Asn Gly Ala Gly Leu
325 330 335

Gly Gln Pro Pro Gln Ala Ser Pro Thr Asp Phe Pro Asn Ala His Leu
340 345 350

Asp Ala Tyr Val Trp Ile Lys Pro Pro Gly Glu Ser Asp Gly Thr Ser
355 360 365

Ala Ala Ser Asp Pro Thr Thr Gly Lys Lys Ser Asp Pro Met Cys Asp
370 375 380

Pro Thr Tyr Thr Thr Ser Tyr Gly Val Leu Thr Asn Ala Leu Pro Asn
385 390 395 400

Ser Pro Ile Ala Gly Gln Trp Phe Pro Ala Gln Phe Asp Gln Leu Val
405 410 415

Ala Asn Ala Arg Pro Ala Val
420

<210> 5

<211> 150

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Segment of
GuxA

<400> 5

Val Ser Gly Gly Leu Lys Val Gln Tyr Lys Asn Asn Asp Ser Ala Pro
1 5 10 15

Gly Asp Asn Gln Ile Lys Pro Gly Leu Gln Leu Val Asn Thr Gly Ser
20 25 30

Ser Ser Val Asp Leu Ser Thr Val Thr Val Arg Tyr Trp Phe Thr Arg
35 40 45

Asp Gly Gly Ser Ser Thr Leu Val Tyr Asn Cys Asp Trp Ala Ala Met
50 55 60

Gly Cys Gly Asn Ile Arg Ala Ser Phe Gly Ser Val Asn Pro Ala Thr
65 70 75 80

Pro Thr Ala Asp Thr Tyr Leu Gln Leu Ser Phe Thr Gly Gly Thr Leu
85 90 95

Ala Ala Gly Gly Ser Thr Gly Glu Ile Gln Asn Arg Val Asn Lys Ser
100 105 110

Asp Trp Ser Asn Phe Thr Glu Thr Asn Asp Tyr Ser Tyr Gly Thr Asn
115 120 125

Thr Thr Phe Gln Asp Trp Thr Lys Val Thr Val Tyr Val Asn Gly Val
130 135 140

Leu Val Trp Gly Thr Glu
145 150

<210> 6

<211> 85

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Segment of
GuxA

<400> 6

Asp Val Thr Pro Pro Ser Val Pro Thr Gly Leu Val Val Thr Gly Val
1 5 10 15

Ser Gly Ser Ser Val Ser Leu Ala Trp Asn Ala Ser Thr Asp Asn Val
20 25 30

Gly Val Ala His Tyr Asn Val Tyr Arg Asn Gly Val Leu Val Gly Gln
35 40 45

Pro Thr Val Thr Ser Phe Thr Asp Thr Gly Leu Ala Ala Gly Thr Ala
50 55 60

Tyr Thr Tyr Thr Val Ala Ala Val Asp Ala Ala Gly Asn Thr Ser Ala
65 70 75 80

Pro Ser Thr Pro Val
85

<210> 7
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Segment of
GuxA

<400> 7
Asp Cys Thr Pro Gly Pro Asn Gln Asn Gly Val Thr Ser Val Gln Gly
1 5 10 15

Asp Glu Tyr Arg Val Gln Thr Asn Glu Trp Asn Ser Ser Ala Gln Gln
20 25 30

Cys Leu Thr Ile Asn Thr Ala Thr Gly Ala Trp Thr Val Ser Thr Ala
35 40 45

Asn Phe Ser Gly Gly Thr Gly Gly Ala Pro Ala Thr Tyr Pro Ser Ile
50 55 60

Tyr Lys Gly Cys His Trp Gly Asn Cys Thr Thr Lys Asn Val Gly Met
65 70 75 80

Pro Ile Gln Ile Ser Gln Ile Gly Ser Ala Val Thr Ser Trp Ser Thr
85 90 95

Thr Gln Val Ser Ser Gly Ala Tyr Asp Val Ala Tyr Asp Ile Trp Thr
100 105 110

Asn Ser Thr Pro Thr Thr Thr Gly Gln Pro Asn Gly Thr Glu Ile Met
115 120 125

Ile Trp Leu Asn Ser Arg Gly Gly Val Gln Pro Phe Gly Ser Gln Thr
130 135 140

Ala Thr Gly Val Thr Val Ala Gly His Thr Trp Asn Val Trp Gln Gly
145 150 155 160

Gln Gln Thr Ser Trp Lys Ile Ile Ser Tyr Val Leu Thr Pro Gly Ala
165 170 175

Thr Ser Ile Ser Asn Leu Asp Leu Lys Ala Ile Phe Ala Asp Ala Ala
180 185 190

Ala Arg Gly Ser Leu Asn Thr Ser Asp Tyr Leu Leu Asp Val Glu Ala
195 200 205

Gly Phe Glu Ile Trp Gln Gly Gly Gln Gly Leu Gly Ser Asn Ser Phe
210 215 220

Ser Val Ser Val Thr Ser Gly
225 230

<210> 8

<211> 101

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Segment of
GuxA

<400> 8

Gly Val Ala Cys Arg Ala Thr Tyr Val Val Asn Ser Asp Trp Gly Ser
1 5 10 15

Gly Phe Thr Ala Thr Val Thr Val Thr Asn Thr Gly Ser Arg Ala Thr
20 25 30

Asn Gly Trp Thr Val Ala Trp Ser Phe Gly Gly Asn Gln Thr Val Thr
35 40 45

Asn Tyr Trp Asn Thr Ala Leu Thr Gln Ser Gly Ala Ser Val Thr Ala
50 55 60

Thr Asn Leu Ser Tyr Asn Asn Val Ile Gln Pro Gly Gln Ser Thr Thr
65 70 75 80

Phe Gly Phe Asn Gly Ser Tyr Ser Gly Thr Asn Ala Ala Pro Thr Leu
85 90 95

Ser Cys Thr Ala Ser
100

<210> 9

<211> 423

<212> PRT

<213> Acidothermus cellulolyticus

<400> 9

Ala Thr His Val Asp Asn Pro Tyr Ala Gly Ala Thr Phe Phe Val Asn
1 5 10 15

Pro Tyr Trp Ala Gln Glu Val Gln Ser Glu Ala Ala Asn Gln Thr Asn
20 25 30

Ala Thr Leu Ala Ala Lys Met Arg Val Val Ser Thr Tyr Ser Thr Ala
35 40 45

Val Trp Met Asp Arg Ile Ala Ala Ile Asn Gly Val Asn Gly Gly Pro
50 55 60

Gly Leu Thr Thr Tyr Leu Asp Ala Ala Leu Ser Gln Gln Gln Gly Thr
65 70 75 80

Thr Pro Glu Val Ile Glu Ile Val Ile Tyr Asp Leu Pro Gly Arg Asp
85 90 95

Cys Ala Ala Leu Ala Ser Asn Gly Glu Leu Pro Ala Thr Ala Ala Gly
100 105 110

Leu Gln Thr Tyr Glu Thr Gln Tyr Ile Asp Pro Ile Ala Ser Ile Leu
115 120 125

Ser Asn Pro Lys Tyr Ser Ser Leu Arg Ile Val Thr Ile Ile Glu Pro
130 135 140

Asp Ser Leu Pro Asn Ala Val Thr Asn Met Ser Ile Gln Ala Cys Ala
145 150 155 160

Thr Ala Val Pro Tyr Tyr Glu Gln Gly Ile Glu Tyr Ala Leu Thr Lys
165 170 175

Leu His Ala Ile Pro Asn Val Tyr Ile Tyr Met Asp Ala Ala His Ser
180 185 190

Gly Trp Leu Gly Trp Pro Asn Asn Ala Ser Gly Tyr Val Gln Glu Val
195 200 205

Gln Lys Val Leu Asn Ala Ser Ile Gly Val Asn Gly Ile Asp Gly Phe
210 215 220

Val Thr Asn Thr Ala Asn Tyr Thr Pro Leu Lys Glu Pro Phe Met Thr
225 230 235 240

Ala Thr Gln Gln Val Gly Gly Gln Pro Val Glu Ser Ala Asn Phe Tyr
245 250 255

Gln Trp Asn Pro Asp Ile Asp Glu Ala Asp Tyr Ala Val Asp Leu Tyr
260 265 270

Ser Arg Leu Val Ala Ala Gly Phe Pro Ser Ser Ile Gly Met Leu Ile
275 280 285

Asp Thr Leu Arg Asn Gly Trp Gly Gly Pro Asn Glu Pro Thr Gly Pro
290 295 300

Ser Thr Ala Thr Asp Val Asn Thr Phe Val Asn Gln Ser Lys Ile Asp
305 310 315 320

Leu Arg Gln His Arg Gly Leu Trp Cys Asn Gln Asn Gly Ala Gly Leu
325 330 335

Gly Gln Pro Pro Gln Ala Ser Pro Thr Asp Phe Pro Asn Ala His Leu
340 345 350

Asp Ala Tyr Val Trp Ile Lys Pro Pro Gly Glu Ser Asp Gly Thr Ser
355 360 365

Ala Ala Ser Asp Pro Thr Thr Gly Lys Lys Ser Asp Pro Met Cys Asp
370 375 380

Pro Thr Tyr Thr Thr Ser Tyr Gly Val Leu Thr Asn Ala Leu Pro Asn
385 390 395 400

Ser Pro Ile Ala Gly Gln Trp Phe Pro Ala Gln Phe Asp Gln Leu Val
405 410 415

Ala Asn Ala Arg Pro Ala Val
420

<210> 10

<211> 430

<212> PRT

<213> Cellulomonas fimi

<400> 10

Ala Pro Val His Val Asp Asn Pro Tyr Ala Gly Ala Val Gln Tyr Val
1 5 10 15

Asn Pro Thr Trp Ala Ala Ser Val Asn Ala Ala Ala Gly Arg Gln Ser
20 25 30

Ala Asp Pro Ala Leu Ala Ala Lys Met Arg Thr Val Ala Gly Gln Pro
35 40 45

Thr Ala Val Trp Met Asp Arg Ile Ser Ala Ile Thr Gly Asn Ala Asp
50 55 60

Gly Asn Gly Leu Lys Phe His Leu Asp Asn Ala Val Ala Gln Gln Lys
65 70 75 80

Ala Ala Gly Val Pro Leu Val Phe Asn Leu Val Ile Tyr Asp Leu Pro
85 90 95

Gly Arg Asp Cys Phe Ala Leu Ala Ser Asn Gly Glu Leu Pro Ala Thr
100 105 110

Asp Ala Gly Leu Ala Arg Tyr Lys Ser Glu Tyr Ile Asp Pro Ile Ala
115 120 125

Asp Leu Leu Asp Asn Pro Glu Tyr Glu Ser Ile Arg Ile Ala Ala Thr
130 135 140

Ile Glu Pro Asp Ser Leu Pro Asn Leu Thr Thr Asn Ile Ser Glu Pro
145 150 155 160

Ala Cys Gln Gln Ala Ala Pro Tyr Tyr Arg Gln Gly Val Lys Tyr Ala
165 170 175

Leu Asp Lys Leu His Ala Ile Pro Asn Val Tyr Asn Tyr Ile Asp Ile
180 185 190

Gly His Ser Gly Trp Leu Gly Trp Asp Ser Asn Ala Gly Pro Ser Ala
195 200 205

Thr Leu Phe Ala Glu Val Ala Lys Ser Thr Thr Ala Gly Phe Ala Ser
210 215 220

Ile Asp Gly Phe Val Ser Asp Val Ala Asn Thr Thr Pro Leu Glu Glu
225 230 235 240

Pro Leu Leu Ser Asp Ser Ser Leu Thr Ile Asn Asn Thr Pro Ile Arg
245 250 255

Ser Ser Lys Phe Tyr Glu Trp Asn Phe Asp Phe Asp Glu Ile Asp Tyr
260 265 270

Thr Ala His Met His Arg Leu Leu Val Ala Ala Gly Phe Pro Ser Ser
275 280 285

Ile Gly Met Leu Val Asp Thr Ser Arg Asn Gly Trp Gly Gly Pro Asn
290 295 300

Arg Pro Thr Ser Ile Thr Ala Ser Thr Asp Val Asn Ala Tyr Val Asp
305 310 315 320

Ala Asn Arg Val Asp Arg Arg Val His Arg Gly Ala Trp Cys Asn Pro
325 330 335

Leu Gly Ala Gly Ile Gly Arg Phe Pro Glu Ala Thr Pro Ser Gly Tyr
340 345 350

Ala Ala Ser His Leu Asp Ala Phe Val Trp Ile Lys Pro Pro Gly Glu
355 360 365

Ser Asp Gly Ala Ser Thr Asp Ile Pro Asn Asp Gln Gly Lys Arg Phe
370 375 380

Asp Arg Met Cys Asp Pro Thr Phe Val Ser Pro Lys Leu Asn Asn Gln
385 390 395 400

Leu Thr Gly Ala Thr Pro Asn Ala Pro Leu Ala Gly Gln Trp Phe Glu
405 410 415

Glu Gln Phe Val Thr Leu Val Lys Asn Ala Tyr Pro Val Ile
420 425 430

<210> 11

<211> 432

<212> PRT

<213> Thermobifida fusca

<400> 11

Pro Gly Gly Pro Thr Asn Pro Pro Thr Asn Pro Gly Glu Lys Val Asp
1 5 10 15

Asn Pro Phe Glu Gly Ala Lys Leu Tyr Val Asn Pro Val Trp Ser Ala
20 25 30

Lys Ala Ala Ala Glu Pro Gly Gly Ser Ala Val Ala Asn Glu Ser Thr
35 40 45

Ala Val Trp Leu Asp Arg Ile Gly Ala Ile Glu Gly Asn Asp Ser Pro
50 55 60

Thr Thr Gly Ser Met Gly Leu Arg Asp His Leu Glu Glu Ala Val Arg
65 70 75 80

Gln Ser Gly Gly Asp Pro Leu Thr Ile Gln Val Val Ile Tyr Asn Leu
85 90 95

Pro Gly Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu Leu Gly Pro
100 105 110

Asp Glu Leu Asp Arg Tyr Lys Ser Glu Tyr Ile Asp Pro Ile Ala Asp
115 120 125

Ile Met Trp Asp Phe Ala Asp Tyr Glu Asn Leu Arg Ile Val Ala Ile
130 135 140

Ile Glu Ile Asp Ser Leu Pro Asn Leu Val Thr Asn Val Gly Gly Asn
145 150 155 160

Gly Gly Thr Glu Leu Cys Ala Tyr Met Lys Gln Asn Gly Gly Tyr Val
165 170 175

Asn Gly Val Gly Tyr Ala Leu Arg Lys Leu Gly Glu Ile Pro Asn Val
180 185 190

Tyr Asn Tyr Ile Asp Ala Ala His His Gly Trp Ile Gly Trp Asp Ser
195 200 205

Asn Phe Gly Pro Ser Val Asp Ile Phe Tyr Glu Ala Ala Asn Ala Ser
210 215 220

Gly Ser Thr Val Asp Tyr Val His Gly Phe Ile Ser Asn Thr Ala Asn
225 230 235 240

Tyr Ser Ala Thr Val Glu Pro Tyr Leu Asp Val Asn Gly Thr Val Asn
245 250 255

Gly Gln Leu Ile Arg Gln Ser Lys Trp Val Asp Trp Asn Gln Tyr Val
260 265 270

Asp Glu Leu Ser Phe Val Gln Asp Leu Arg Gln Ala Leu Ile Ala Lys
275 280 285

Gly Phe Arg Ser Asp Ile Gly Met Leu Ile Asp Thr Ser Arg Asn Gly
290 295 300

Trp Gly Gly Pro Asn Arg Pro Thr Gly Pro Ser Ser Ser Thr Asp Leu
305 310 315 320

Asn Thr Tyr Val Asp Glu Ser Arg Ile Asp Arg Arg Ile His Pro Gly
325 330 335

Asn Trp Cys Asn Gln Ala Gly Ala Gly Leu Gly Glu Arg Pro Thr Val
340 345 350

Asn Pro Ala Pro Gly Val Asp Ala Tyr Val Trp Val Lys Pro Pro Gly
355 360 365

Glu Ser Asp Gly Ala Ser Glu Glu Ile Pro Asn Asp Glu Gly Lys Gly
370 375 380

Phe Asp Arg Met Cys Asp Pro Thr Tyr Gln Gly Asn Ala Arg Asn Gly
385 390 395 400

Asn Asn Pro Ser Gly Ala Leu Pro Asn Ala Pro Ile Ser Gly His Trp
405 410 415

Phe Ser Ala Gln Phe Arg Glu Leu Leu Ala Asn Ala Tyr Pro Pro Leu
420 425 430

<210> 12

<211> 221

<212> PRT

<213> Acidothermus cellulolyticus

<400> 12

Asn Gln Gln Ile Cys Asp Arg Tyr Gly Thr Thr Thr Ile Gln Asp Arg
1 5 10 15

Tyr Val Val Gln Asn Asn Arg Trp Gly Thr Ser Ala Thr Gln Cys Ile
20 25 30

Asn Val Thr Gly Asn Gly Phe Glu Ile Thr Gln Ala Asp Gly Ser Val
35 40 45

Pro Thr Asn Gly Ala Pro Lys Ser Tyr Pro Ser Val Tyr Asp Gly Cys
50 55 60

His Tyr Gly Asn Cys Ala Pro Arg Thr Thr Leu Pro Met Arg Ile Ser
65 70 75 80

Ser Ile Gly Ser Ala Pro Ser Ser Val Ser Tyr Arg Tyr Thr Gly Asn
85 90 95

Gly Val Tyr Asn Ala Ala Tyr Asp Ile Trp Leu Asp Pro Thr Pro Arg
100 105 110

Thr Asn Gly Val Asn Arg Thr Glu Ile Met Ile Trp Phe Asn Arg Val
115 120 125

Gly Pro Val Gln Pro Ile Gly Ser Pro Val Gly Thr Ala His Val Gly
130 135 140

Gly Arg Ser Trp Glu Val Trp Thr Gly Ser Asn Gly Ser Asn Asp Val
145 150 155 160

Ile Ser Phe Leu Ala Pro Ser Ala Ile Ser Ser Trp Ser Phe Asp Val
165 170 175

Lys Asp Phe Val Asp Gln Ala Val Ser His Gly Leu Ala Thr Pro Asp
180 185 190

Trp Tyr Leu Thr Ser Ile Gln Ala Gly Phe Glu Pro Trp Glu Gly Gly
195 200 205

Thr Gly Leu Ala Val Asn Ser Phe Ser Ser Ala Val Asn
210 215 220

<210> 13
<211> 221
<212> PRT
<213> Streptomyces sp.

<400> 13

Asp Thr Thr Ile Cys Glu Pro Phe Gly Thr Thr Thr Ile Gln Gly Arg
1 5 10 15

Tyr Val Val Gln Asn Asn Arg Trp Gly Ser Thr Ala Pro Gln Cys Val
20 25 30

Thr Ala Thr Asp Thr Gly Phe Arg Val Thr Gln Ala Asp Gly Ser Ala
35 40 45

Pro Thr Asn Gly Ala Pro Lys Ser Tyr Pro Ser Val Phe Asn Gly Cys
50 55 60

His Tyr Thr Asn Cys Ser Pro Gly Thr Asp Leu Pro Val Arg Leu Asp
65 70 75 80

Thr Val Ser Ala Ala Pro Ser Ser Ile Ser Tyr Gly Phe Val Asp Gly
85 90 95

Ala Val Tyr Asn Ala Ser Tyr Asp Ile Trp Leu Asp Pro Thr Ala Arg
100 105 110

Thr Asp Gly Val Asn Gln Thr Glu Ile Met Ile Trp Phe Asn Arg Val
115 120 125

Gly Pro Ile Gln Pro Ile Gly Ser Pro Val Gly Thr Ala Ser Val Gly
130 135 140

Gly Arg Thr Trp Glu Val Trp Ser Gly Gly Asn Gly Ser Asn Asp Val
145 150 155 160

Leu Ser Phe Val Ala Pro Ser Ala Ile Ser Gly Trp Ser Phe Asp Val
165 170 175

Met Asp Phe Val Arg Ala Thr Val Ala Arg Gly Leu Ala Glu Asn Asp
180 185 190

Trp Tyr Leu Thr Ser Val Gln Ala Gly Phe Glu Pro Trp Gln Asn Gly
195 200 205

Ala Gly Leu Ala Val Asn Ser Phe Ser Ser Thr Val Glu
210 215 220

<210> 14
<211> 228
<212> PRT
<213> Streptomyces lividans

<400> 14
Cys Thr Pro Gly Pro Asn Gln Asn Gly Val Thr Ser Val Gln Gly Asp
1 5 10 15
Glu Tyr Arg Val Gln Thr Asn Glu Trp Asn Ser Ser Ala Gln Gln Cys
20 25 30
Leu Thr Ile Asn Thr Ala Thr Gly Ala Trp Thr Val Ser Thr Ala Asn
35 40 45
Phe Ser Gly Gly Thr Gly Gly Ala Pro Ala Thr Tyr Pro Ser Ile Tyr
50 55 60
Lys Gly Cys His Trp Gly Asn Cys Thr Thr Lys Asn Val Gly Met Pro
65 70 75 80
Ile Gln Ile Ser Gln Ile Gly Ser Ala Val Thr Ser Trp Ser Thr Thr
85 90 95
Gln Val Ser Ser Gly Ala Tyr Asp Val Ala Tyr Asp Ile Trp Thr Asn
100 105 110
Ser Thr Pro Thr Thr Thr Gly Gln Pro Asn Gly Thr Glu Ile Met Ile
115 120 125
Trp Leu Asn Ser Arg Gly Gly Val Gln Pro Phe Gly Ser Gln Thr Ala
130 135 140
Thr Gly Val Thr Val Ala Gly His Thr Trp Asn Val Trp Gln Gly Gln
145 150 155 160
Gln Thr Ser Trp Lys Ile Ile Ser Tyr Val Leu Thr Pro Gly Ala Thr
165 170 175
Ser Ile Ser Asn Leu Asp Leu Lys Ala Ile Phe Ala Asp Ala Ala Ala
180 185 190
Arg Gly Ser Leu Asn Thr Ser Asp Tyr Leu Leu Asp Val Glu Ala Gly
195 200 205
Phe Glu Ile Trp Gln Gly Gly Gln Gly Leu Gly Ser Asn Ser Phe Ser
210 215 220
Val Ser Val Thr
225